

Ecography

ECOG-05024

Boulanger, E., Dalongeville, A., Andrello, M., Mouillot, D. and Manel, S. 2020. Spatial graphs highlight how multi-generational dispersal shapes landscape genetic patterns. – Ecography doi: 10.1111/ecog.05024

Supplementary material

Spatial graphs for seascape genetics
SUPPLEMENTARY MATERIAL

Appendix 1

Tables

Table A1. Network-level comparison of the realized (genetic) connectivity spatial graph, random graphs with the same number of nodes and edges, and the potential (larval dispersal probability) connectivity graph.

	Genetic connectivity (pruned graph)	Random ^a	Larval connectivity
Topology	Mostly across-basin connectivity	random	Mostly within-basin connectivity
Assortativity <i>r</i>	-0.57	-0.05 ± 0.09	0.34
Clustering <i>c</i>	0.58	0.10 ± 0.02	0.58

^a mean ± standard deviation

Figures

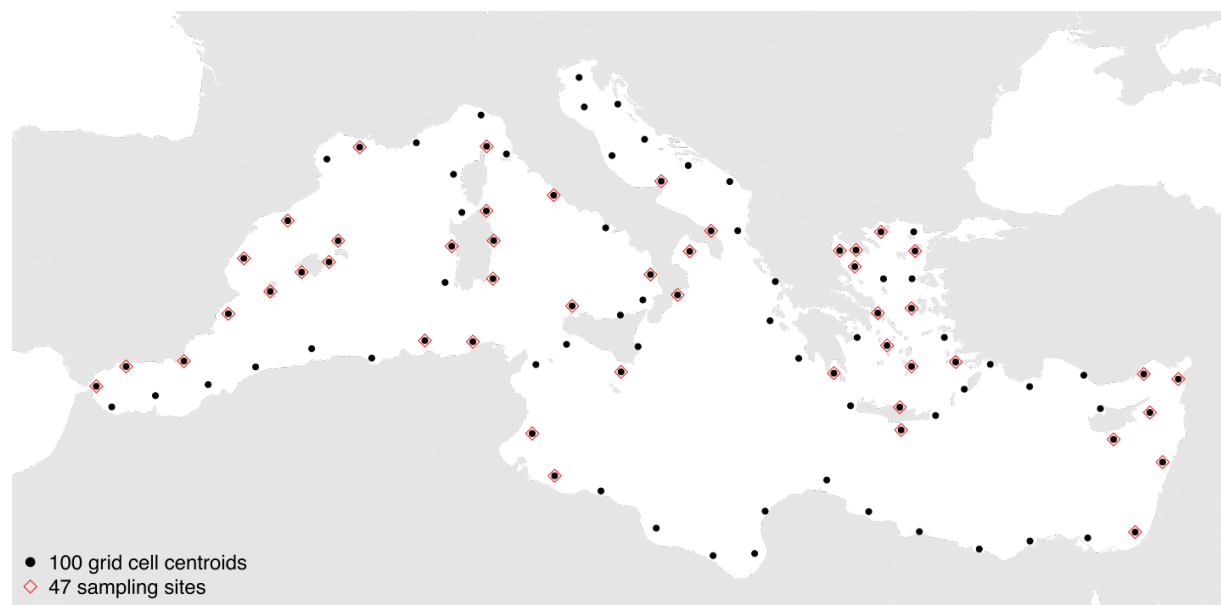


Figure A1. Location of the 100 grid cell centroids of the larval dispersal model and the 47 population sites extracted from the model grid cells.

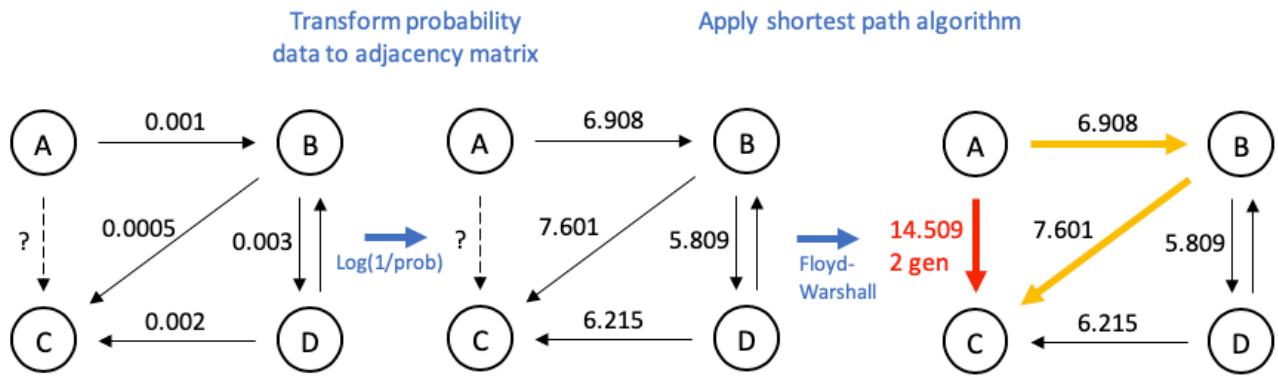


Figure A2. Schematic representation of the stepping-stone approach to multi-generational larval dispersal. If no direct connection exists (i.e. larval dispersal probability = 0) between the nodes A and C, shortest path algorithms can identify the multistep connection from A → B → C. The biological interpretation is that it would take at least two generations to disperse from node A to C through larval dispersal.

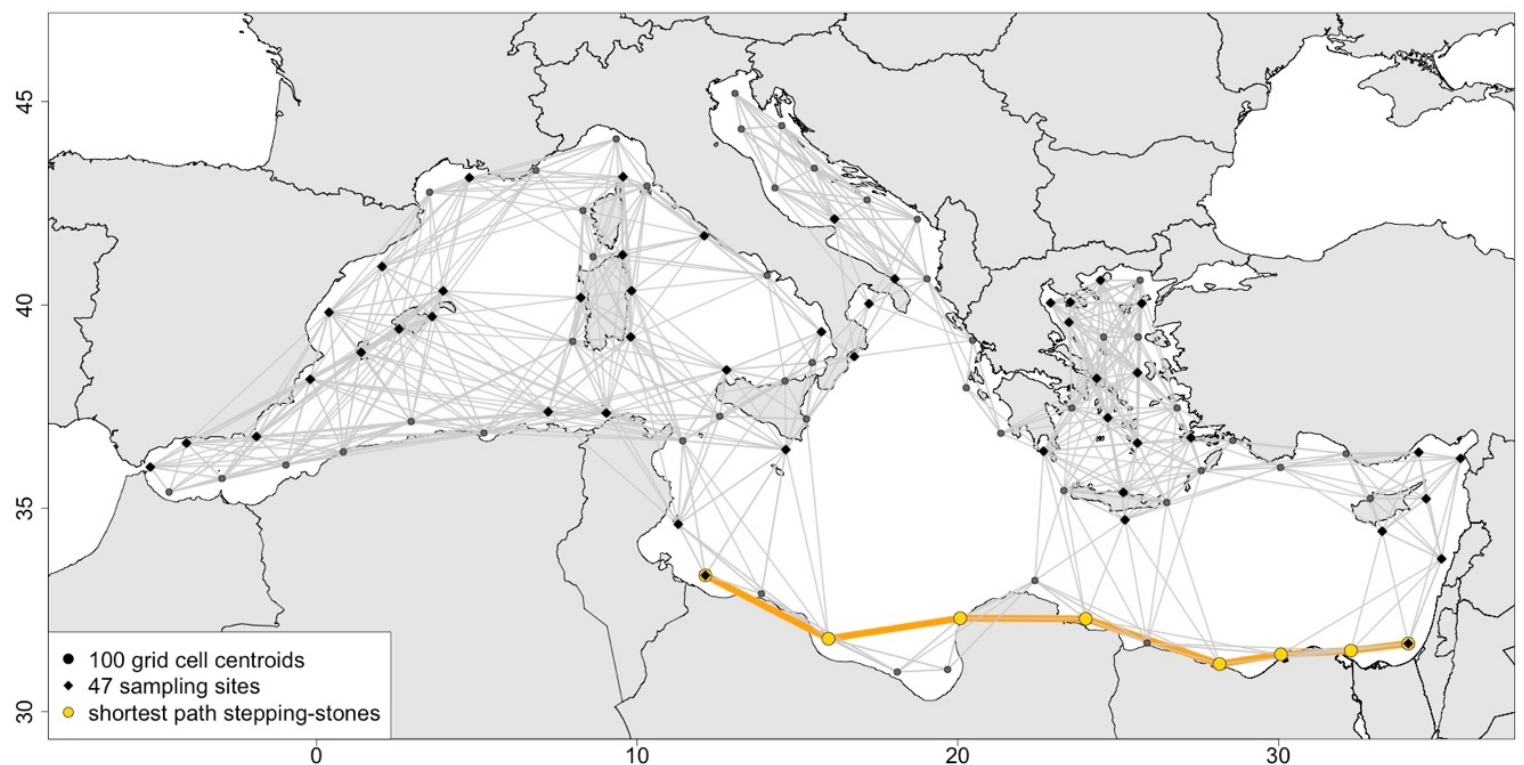


Figure A3. Illustration of how the shortest paths are calculated using the single-generation larval dispersal probabilities (light grey edges) between the 100 grid cell centroids (black dots) and then extracted for the 47 population sites (black diamonds). This way, unsampled sites that act as stepping-stones for dispersal between the 47 sampled population sites are considered in the assessment of multi-generational dispersal. The shortest path (gold) connecting the sampled populations 91 (Libya) and 74 (Israel) passes through unsampled sites along the North-African coast.

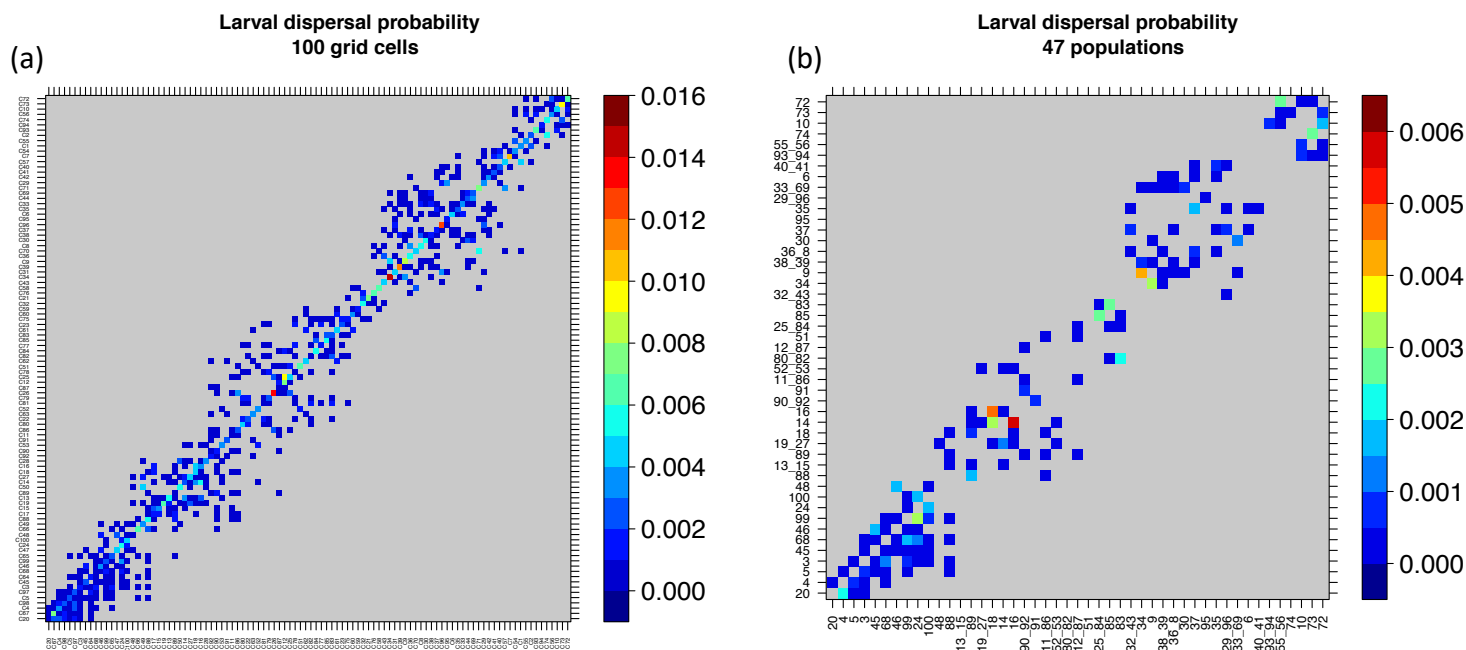


Figure A4. Levelplot of the larval dispersal matrices between the 100 grid cell centroids (a) and the 47 sampled populations (b). Cells and populations are ordered by longitude.

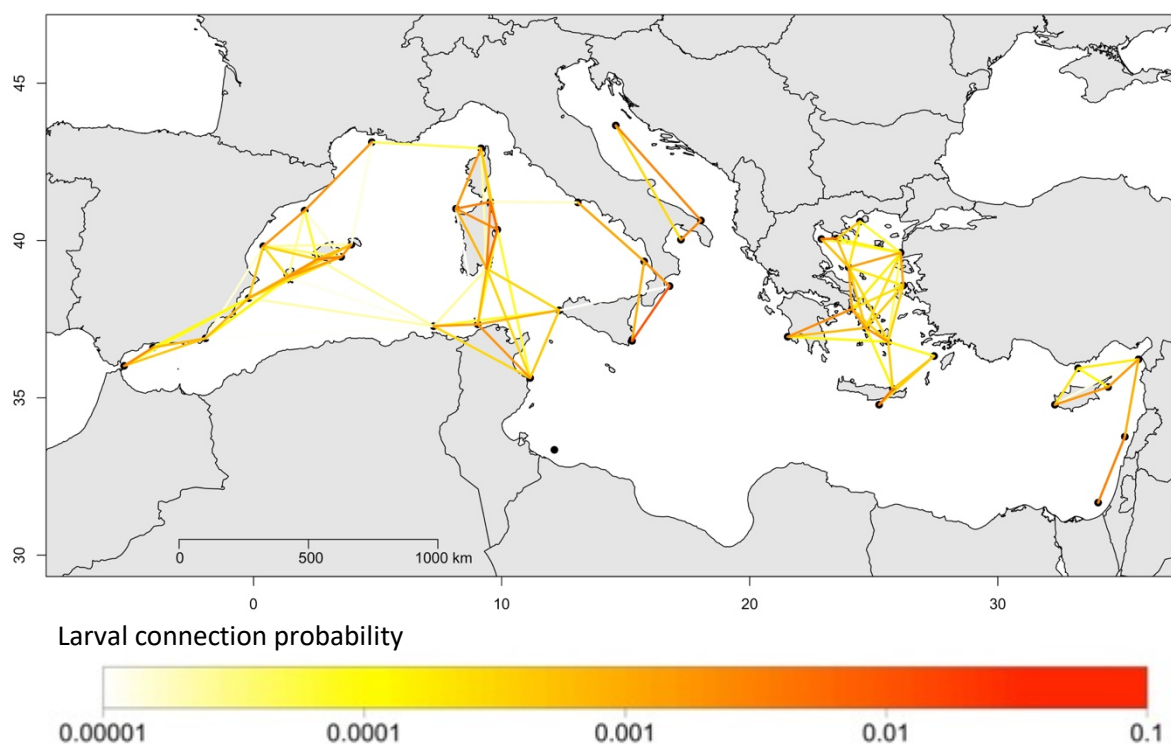


Figure A5. Spatial graph of modelled larval connection probabilities between the 47 sampling sites.

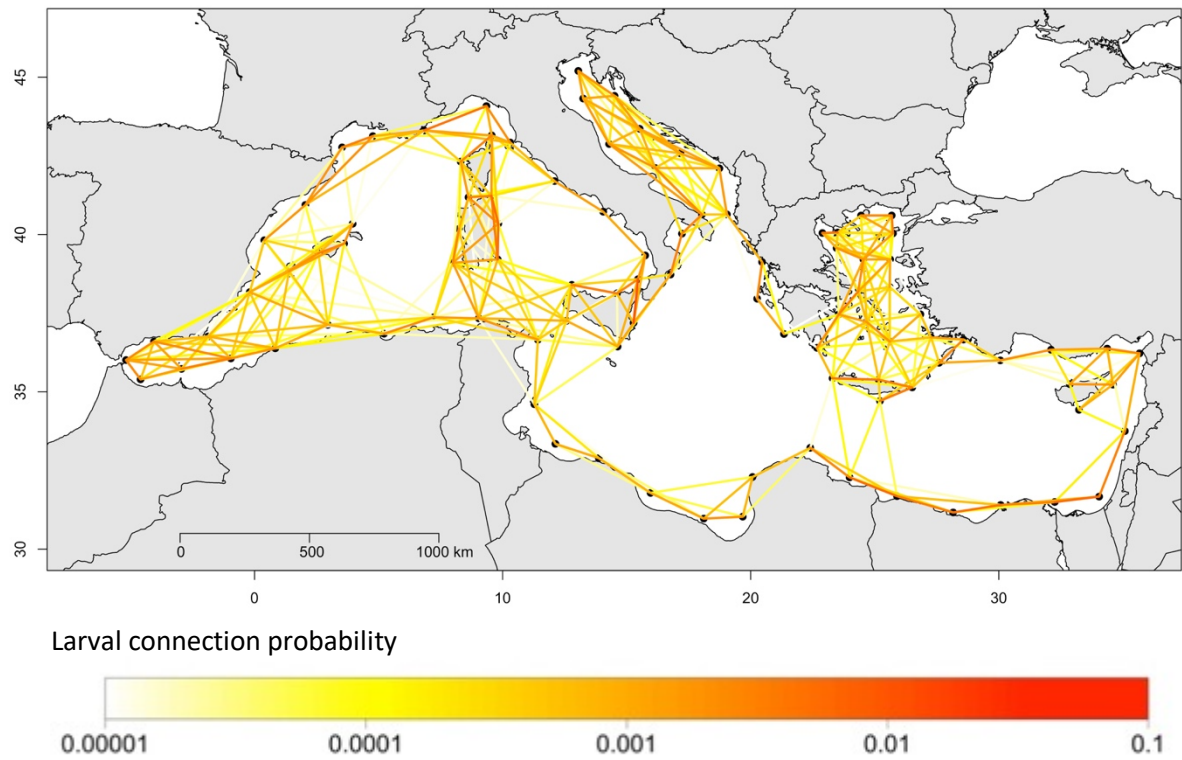


Figure A6. Spatial graph of the direct larval connection probabilities between the 100 modelled sites.

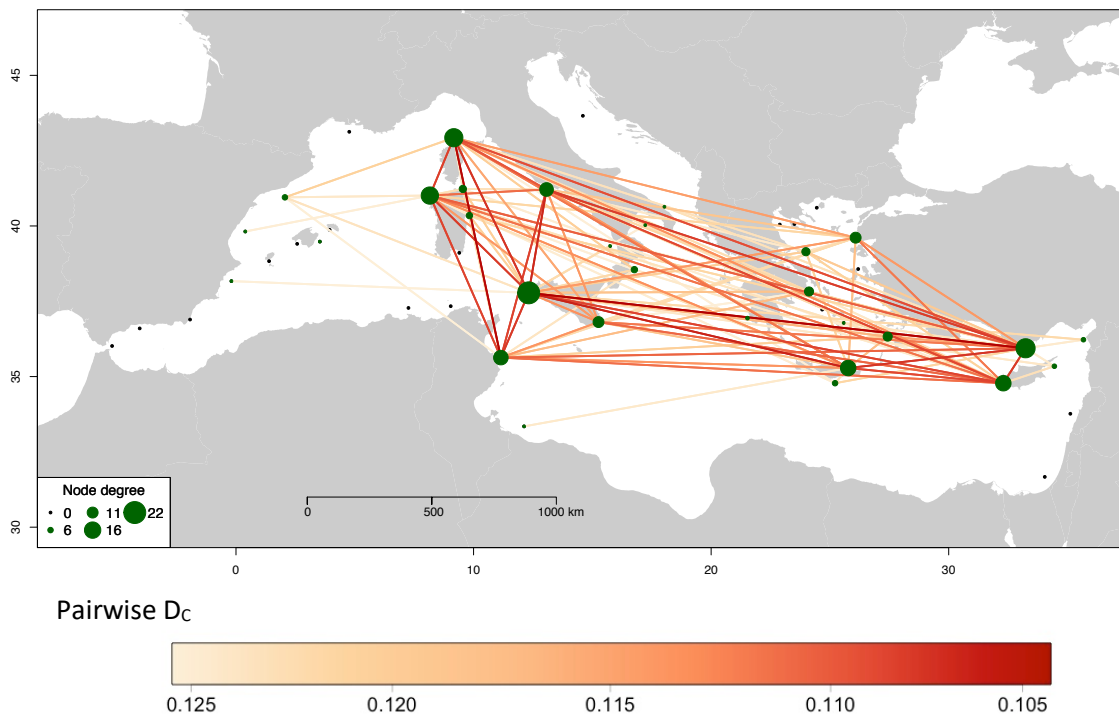


Figure A7. Spatial graph representing the genetic connectivity network of *Mullus surmuletus* in the Mediterranean Sea. Edges between nodes (populations) are weighted by their pairwise genetic distance (D_c), represented by a colour gradient. The size of nodes is proportional to their degree.

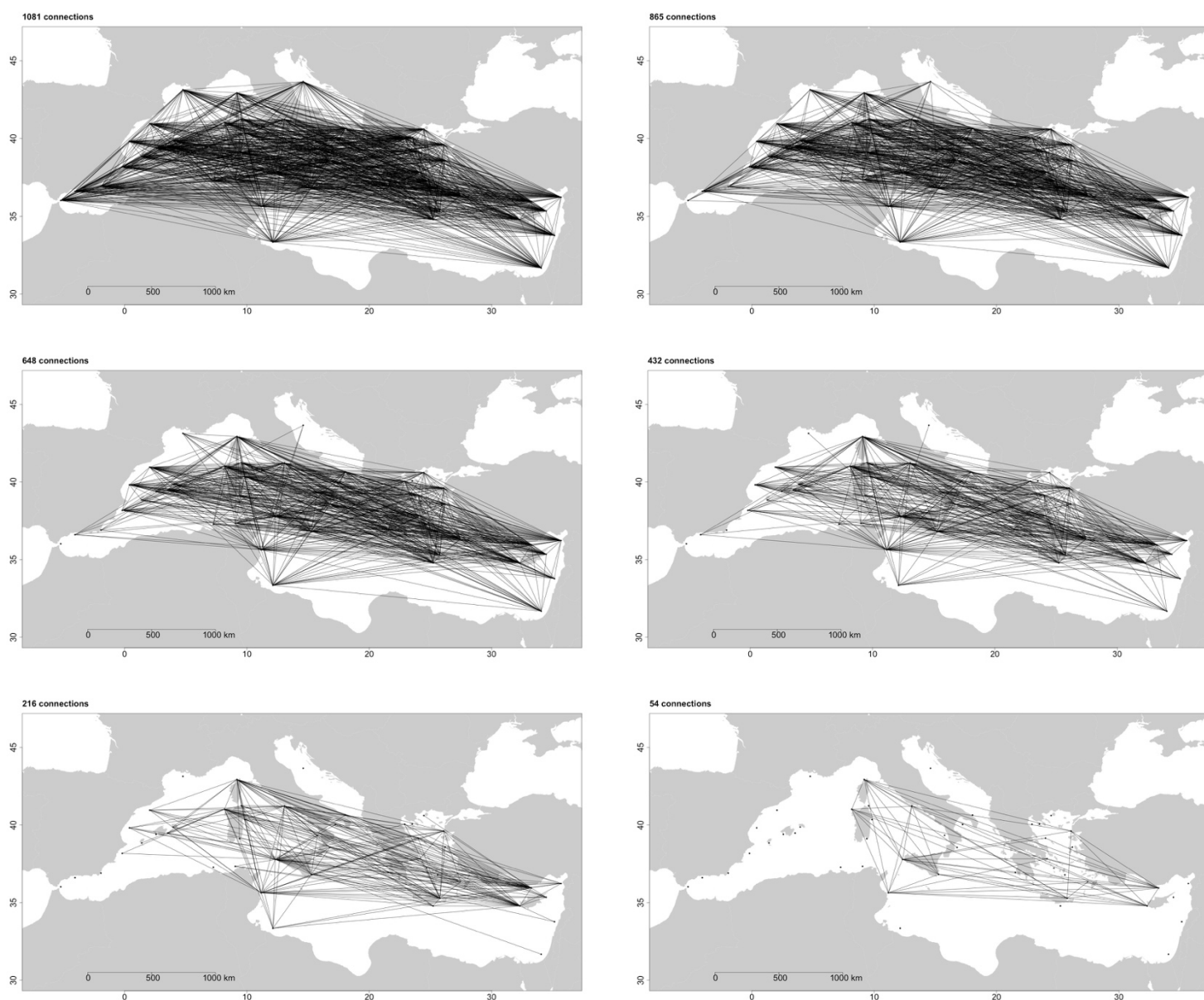


Figure A8. Edge removal scenario showing 100%, 80%, 60%, 40, 20, 5% of all possible connections respectively. Edges were pruned sequentially by decreasing genetic distance.

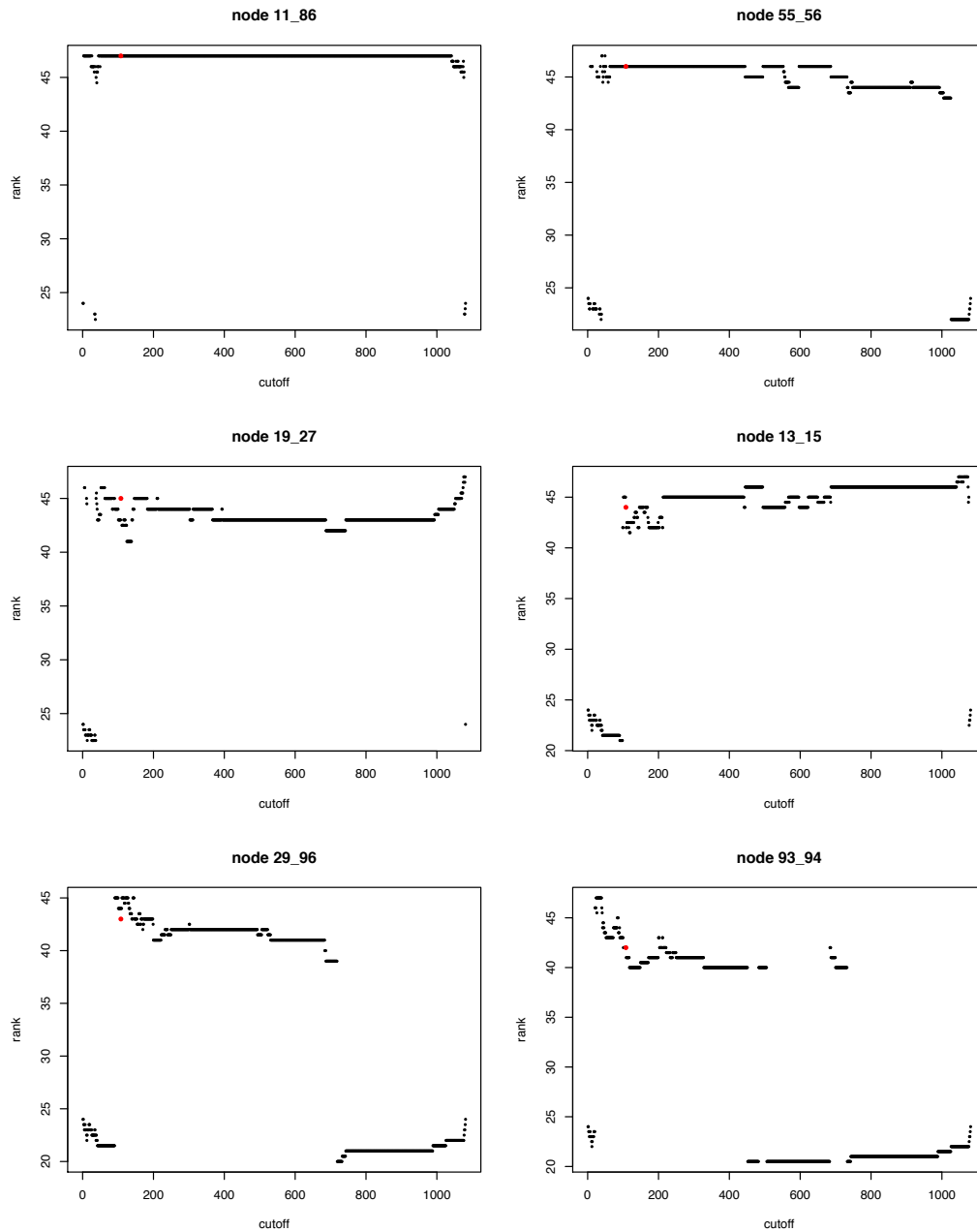


Figure A9 : Ranking of nodes in the genetic connectivity spatial graph based on their betweenness value for varying thresholds. The red point corresponds to the betweenness value of the corresponding node in the final genetic connectivity spatial graph.